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| (54) Title: GENETIC ANALYSIS (57) Abstract A method is described for use in whole genome analysis. The method – termed inter–population perfectly matched duplex depletion – can overcome many of the limitations of current approaches based upon SNPs and linkage disequilibrium within isolated populations. Inter–population perfectly matched duplex depletion isolates a fragment (or fragments) containing differences between the "affected" and "unaffected" populations or cells. A convenient method – terminal restriction site profiling arrays (TRSPAs) – is described for the analysis of such fragments. A totally diagnostic internal control DNA is also described which allows both the extent and exact nature of any partial digestion to be unambiguously determined for inter–population perfectly matched duplex depletion or TRSPA restriction. | | |

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